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<p>(54) Title: TEMPLATE ASSEMBLED SYNTHETIC PROTEIN</p> <p>(57) Abstract</p> <p>A chemoselective ligation approach to the preparation of complex peptides is employed in a simple, convenient synthesis of template-assembled synthetic protein (TASP) molecules. Reaction of readily prepared synthetic <i>pro</i>-helical peptide-αCOSH molecules, in unprotected form, with a synthetic (BrAc)₄template peptide molecule, also in unprotected form, proceeds rapidly in aqueous solution to give a uniform product in high yield. The resulting TASP molecule may be simply purified to homogeneity. Structural homogeneity may be demonstrated by ionspray mass spectrometry. The chemoselective ligation of unprotected peptides represents a general approach to the synthesis of TASP molecules.</p> <p style="text-align: right;">Serial No.: 09/144,838 Inventor: Siani et al. Attny Docket No. GRFN-020/01US</p> <p style="text-align: right;">F5</p>		

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TEMPLATE ASSEMBLED SYNTHETIC PROTEIN

Technical Field:

5 The invention relates to the synthesis of branched or dendritic peptides. More particularly, the invention relates to the synthesis of template assembled synthetic protein (TASP) molecules using chemoselective ligation procedures and to the genus of TASP's which employ dendritic linkage units having the
10 structure $\psi(\text{CO-S-CH}_2\text{-CO-NH})$.

Background Art:

15 Since the time of Emil Fischer, it has been a goal of organic chemists to design and chemically synthesize proteins. In recent years there has been a growing interest in the *de novo* design of proteins, particularly helix-bundle proteins, and their production by means of chemical synthesis or recDNA-expression. Examples of helix-bundle proteins
20 designed *de novo* are provided by M. Hecht et al. (*Science*, 1990, vol. 249, pages 884-891), by L. Regan et al. (*Science*, 1988, vol. 241, pages 976-978), by W. F. DeGrado et al. (*Science*, 1989, vol. 243, pages 622-628), and by N.E. Zhou et al. (*Biochemistry*, 1992, vol. 31, pages 5739-5746).
25

In some cases, unexpected results have been obtained in which the experimentally observed structure of synthetic helix bundles has been different than the intended structure because of the uncontrolled nature
30 of non-covalent intermolecular association, e.g., see B. Lovejoy et al. (*Science*, 1993, vol. 259, pages 1288-1293). To avoid such problems, helix bundle proteins have been made by the preparation of covalent arrays linked through porphyrin molecules or through
35 metal chelate complexes. Preliminary evidence indicates that the expected structures have been achieved, e.g., see T. Sasaki et al. (*J. Am. Chem. Soc.*, 1989, vol. 111, pages 380-381) and R. M. Ghadiri

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et al. (*J. Am. Chem. Soc.*, 1992, vol. 114, pages 4000-4002).

5 An alternative, earlier approach to the preparation of covalent peptide arrays of predetermined secondary and tertiary structure is the "template assembled synthetic protein" (TASP) concept, disclosed by M. Mutter (*Peptides-Chemistry and Biology, Proceedings of the 10th American Peptide Symposium; Marshall, G. R., Ed.; Escom: Leiden, 1988; pages 10 349-353*). A template molecule is used to covalently anchor arrays of secondary structural elements. The distinctive feature of the TASP approach is the nonlinear topology used; the molecule is made up of an array of branched polypeptides, rather than the folded 15 linear polypeptide chain of natural proteins, e.g., M. Mutter et al., (*Angew. Chem., Int. Ed. Engl.*, 1989, vol. 28, pages 535-554). It is anticipated that this elegant concept will have a profound effect on the *de novo* design of proteins.

20 However, conventional synthetic approaches for preparing TASP molecular assemblies are arduous and/or provide low yields. For example, both stepwise solid phase synthesis (SPPS) and protected segment condensation approaches have been employed with limited 25 success. M. Mutter, M. et al. (*J. Am. Chem. Soc.*, 1992, vol. 114, pages 1463-1470) discloses an example of a stepwise solid phase synthesis (SPPS) of a template assembled synthetic protein. In addition, B. Dorner et al. (*Innovation and Perspectives in Solid 30 Phase Synthesis*, Roger Epton Ed.; Intercept Limited: Andover, 1992; pages 163-170) and by I. Ernest et al. (*Tetrahedron Lett.*, 1990. vol. 31, pages 4015-4018) disclose examples of the protected segment condensation approach for synthesizing template assembled synthetic 35 proteins. Only a minimal number of TASP molecules have been produced by arduous synthetic efforts, e.g. supra and M. Mutter et al. (*Proteins*, 1989, vol. 5, pages 13-21) and G. Tuchscherer (*Protein Science*, 1992, vol.

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1, pages 1377-1386). Despite the exquisite care with which some of these syntheses have been performed, questions still remain with respect to TASP preparations as homogeneous molecular species of defined covalent composition. A convenient, direct general preparation of these molecules in unambiguous fashion would have great utility.

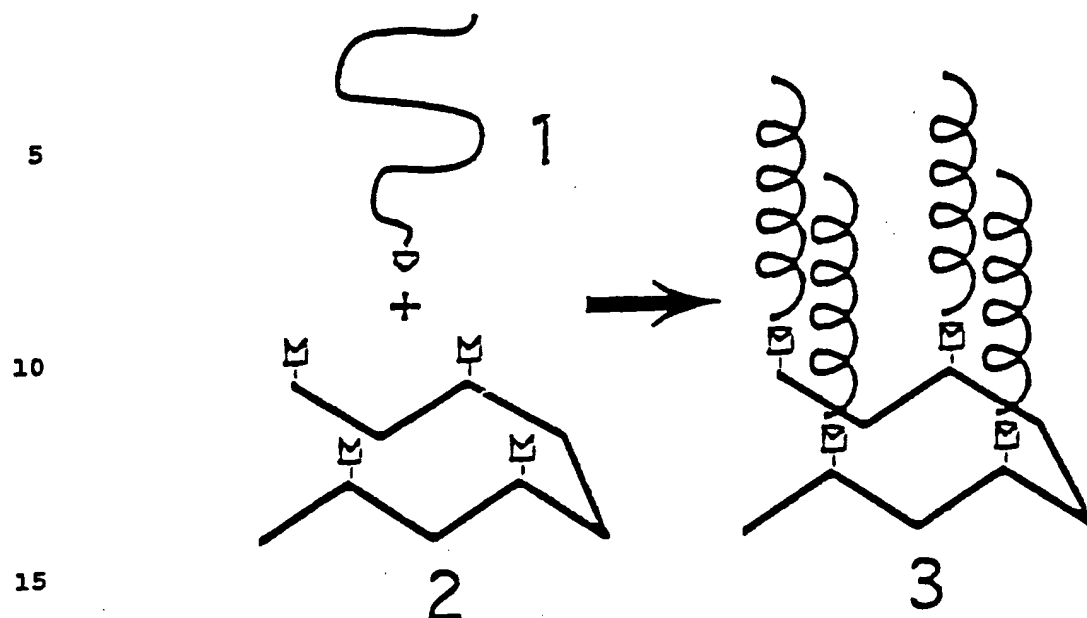
Recently, M. Schnolzer introduced the chemoselective ligation of unprotected peptide segments as a route to the total chemical synthesis of protein analogs of native (i.e. linear) topology (*Science*, 1992, vol. 256, pages 221-225). This approach uses unique, mutually reactive functionalities, one type on each segment, to covalently assemble long chain molecules from completely unprotected peptide segments. In this way, maximal advantage is taken of our ability to synthesize, handle, purify, and characterize unprotected peptides. Solubility problems are reduced and the target molecule is produced directly in the final unprotected form.

Disclosure of the Invention:

The invention employs a chemoselective ligation approach in the synthesis of TASP molecules. The approach used is shown in Scheme I. The TASP is assembled from short unprotected peptide segments, which are synthesized in straightforward fashion by standard methods and which are readily purified to high levels of homogeneity. The target 4-helix TASP molecule was designed on the basis of the work of Mutter (*Tetrahedron*, 1988, vol. 44, pages 771-785). The final molecule contains a total of four copies of the helix-forming peptide 1, one copy attached to the side chain of each of four lysine residues in a template molecule. The template molecule 2 contains a central Gly-Pro sequence to facilitate the formation of a reverse-turn structure, and to thus promote the association of the helix-forming peptides.

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Scheme 1.

Synthesis of a 4-Helix TASP
by Chemoselective Ligation

Brief Description of the Drawings:

Figures 1 (A) and (B) illustrate examples of unprotected synthetic peptides for use in the TASP synthesis.

Figure 1 (A) illustrates a fourteen residue pro-helix peptide-thiocarboxylate 1, prepared by SPPS on a thioester resin.

Figure 1 (B) illustrates a nine residue peptide template 2, prepared by SPPS using N^oBoc protection and both base- and acid-labile side chain protection to allow differential modification of the side chains. Step (i) employs 50% piperidine in DMF; step (ii) employs bromoacetic anhydride in DCM; step (iii) employs HF/10% p-cresol, 1 hour, 0°C. Details are provided in the Materials and Methods section.

Figures 2 (A) and (B) illustrate a reaction of the

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pro-helix peptide- α -thi carboxylate 1 with the (BrAc) template peptide 2, in aqueous solution at pH 5.

Figure 2 (A) illustrates an analytical HPLC of the reaction mixture after 5 hours of reaction. Positions and original amounts of the reactants, i.e., the branch peptide (1) and the template peptide (2), are indicated by dashed-line peaks. The product 4-helix TASP (3) is indicated by a solid line. Minor components were identified by ionspray mass spectrometry (MS). Peak "a" is a pro-helix peptide- α -carboxylate formed by hydrolysis of the α -thiocarboxylate. Peak "b" is a (pro-helix) $_3$ (BrAc) $_1$ template. Peak "c" is a dimer (pro-helix- α -COS-) $_2$ formed by atmospheric oxidation.

Figure 2 (B) illustrates an analytical HPLC of the reaction mixture after 70 min. Products are labeled and identified as above.

Figure 3 (A) illustrates the ionspray mass spectrometry (MS) of HPLC-purified peak 3. Raw data is shown. The multiple charge states all arise from protonation of a single molecular species having a molecular weight of 6647 Daltons. No significant other species were detected in the HPLC fraction.

Figure 3 (B) illustrates a reconstruction of the total raw MS data to a single charge state.

Figure 4 illustrates the circular dichroism spectrum in water of the HPLC-purified 4-helix TASP product 3 (solid line). Characteristic minima at 220nm and 208 nm and a maximum at 193 nm indicate high helical content for the ligated TASP. Under identical conditions the pro-helix peptide 1 (dotted line) gave a weak featureless spectrum with no indication of helical structure.

Best Mode for Carrying Out the Invention:

The invention is a template assembled synthetic protein (TASP) employing a dendritic linkage unit with a structure $\psi(\text{CO-S-CH}_2\text{-CO-NH})$. More particularly, the TASP includes at least one template peptide and one branch peptide joined to one another using the

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dendritic linkage unit indicated above. The template peptide includes at least one amino acid residue with a template side chain bearing an amino group, preferably a lysine group. The template peptide is coupled to the dendritic linkage unit via the lysine or other side chain bearing an amino group. The branch peptide is coupled to the dendritic linkage unit via its C-terminal. An important aspect of the invention is the chemoselective linkage between the template peptide and the branch peptide, i.e., the structure $\psi(\text{CO-S-CH}_2\text{-CO-NH})$ which couples the C-terminal end of the branch peptide to the template peptide via the amino group of the template side chain. The dendritic linkage unit may be schematically illustrated as follows:

Branch Peptide- $\psi(\text{CO-S-CH}_2\text{-CO-NH})$ -Template Side Chain

Template Peptide,

The ensemble forms a template assembled synthetic protein (TASP).

In a preferred embodiment, the branch peptide is a pro-helical peptide which, upon incorporation into the template assembled synthetic protein (TASP) and exposure to helix promoting conditions, is capable of assuming a helical configuration. A preferred branch peptide has the following sequence, viz. Seq. 1:

$^+\text{NH}_3\text{-D-A-A-T-A-L-A-N-A-L-K-K-L-G-COS-}$

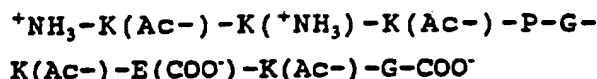
The above branch peptide is a pro-helical peptides which, upon incorporation into a template assembled synthetic protein (TASP) and exposure to helix promoting conditions, is capable of assuming helical configurations. The TASP may include only one branch peptide or may include multiple branch peptides. A preferred TASP includes four branch peptides having Sequence 1. When multiple branch peptides are employed, each branch peptide is coupled to the template peptide via its own dendritic linkage unit.

A preferred template peptide has the following

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sequence, viz. Seq. 2:



wherein K(Ac-) represents a lysine amino acid residue having an lysine side chain with an acetylated amino group.

The invention also contemplates the process for preparing a template assembled synthetic protein (TASP). The process comprises the following steps:

Step A: providing an unprotected template peptide including an amino acid residue having a side chain bearing an amino group bonded to a haloacetyl functionality;

Step B: providing unprotected branch peptides each bearing a $^{\circ}\text{COSH}$ moiety at its C-terminal end; and then

Step C: combining the unprotected template peptide from said Step A with the unprotected branch peptide of said Step B under nucleophilic reaction conditions for promoting a substitution reaction between the $^{\circ}\text{COSH}$ moiety of the branch peptides and the haloacetyl functionalities of the template molecule for chemoselectively ligating the branch peptides to the template peptide and forming the template assembled synthetic protein (TASP).

In a preferred mode of the process, the haloacetyl functionality of the template peptide of Step A is a bromoacetyl group attached to the amino group of a lysine side chain. In Step C, the dendritic linkage unit is formed when the $^{\circ}\text{COSH}$ moiety of the branch peptides and the bromoacetyl group of the template molecule undergo a nucleophilic substitution reaction to create a dendritic linkage unit having the following structure, viz.:



A preferred mode of the process for preparing a TASP may also include an additional step after completion of the assembly for exposing the reaction product to helix promoting conditions for changing the

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conformation of the branch peptides into a helical conformation.

Example:

5 The synthetic peptide 1, intended to form a 13 residue
amphipathic helix under suitable helix-promoting
conditions, was prepared with an additional C-terminal
-Gly^αCOSH residue (Figure 1A). This pro-helix peptide
10 was reacted with the template peptide 2 containing four
lysine side chains modified to contain bromoacetyl
moieties (Figure 1B). Peptides were chemically
synthesized by manual stepwise solid phase methods
according to published procedures, e.g., S. B. Kent
(*Ann Rev Biochem.*, 1988, vol. 57, pages 957-989) and M.
15 Schnolzer et al. (*Int. J. Peptide Protein Res.*, 1992,
vol. 40, pages 180-193). Acidolytic cleavage of the
pro-helix peptide from a thioester resin generates the
peptide-^αCOSH 1, e.g., J. Blake (*Int. J. Peptide Protein
Res.*, 1981, vol. 17, pages 273-274) and D. Yamashiro
20 (*J. Int. J. Peptide Protein Res.*, 1988, vol. 31, pages
322). A combination of base-labile and acid-labile
protecting groups was used to generate the template
molecule 2 with four of the five lysine sidechains
modified with bromoacetyl groups (Figure 1B), e.g., R.
25 A. Robey et al. (*Anal. Biochem.*, 1989, vol. 177, pages
373-377). The range of functionalities present in the
two peptides is shown in Figure 1.

The unprotected peptides were simply ligated in
the desired fashion by nucleophilic reaction between
30 the ^αCOSH moiety of the pro-helix peptide 1 and the
bromoacetyl functionalities of the template molecule 2.
The reaction proceeded cleanly over several hours at
ambient temperature in aqueous buffer at pH 5.0 to give
a near-quantitative yield of the 4-helix TASP molecule
35 3 (Figur 2A). The r action was monitored by direct
ionspray MS of the reaction mixture and by analytical
HPLC, e.g., M. Schnolzer (*Anal. Biochem.*, 1992, vol.
204, pages 335-343). Although salts generally

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interfere with the evaporative ionization process, the dilute NH_4OAc buffer used was compatible with direct ionspray MS of synthetic peptides. An excess of the peptide- $^{\text{C}}\text{OSH}$ component 1 was used, and the final reaction mixture was fully depleted of the $(\text{BrAc})_4$ template molecule 2. The ligation proceeded very quickly as monitored by HPLC. After just 70 minutes, the reaction had progressed almost to completion (Figure 2B). In addition to the target 4-helix TASP 3, the only other detectable components were residual excess pro-helix- $^{\text{C}}\text{OSH}$ 1, residual amounts of $(\text{pro-helix})_3(\text{BrAc})_1$ template, and trace amounts of pro-helix- $^{\text{C}}\text{OOH}$ and the dimer $(\text{pro-helix-}^{\text{C}}\text{OS})_2$. It is of some interest that the only intermediate reaction product detected (Figure 2B) was the $(\text{pro-helix})_3(\text{BrAc})_1$ template.

The desired product was readily purified by HPLC and was lyophilized to yield a white solid. This was characterized by ionspray mass spectrometry (Figure 3) and was found to be the target 4-helix TASP 3 in high purity, and with the expected mass, i.e., the observed molecular weight was 6647.1 ± 2.8 Daltons, while the calculated molecular weight for a monoisotopic $\text{C}_{288}\text{H}_{503}\text{N}_{82}\text{O}_{88}\text{S}_4$ is 6645.6 and the calculated molecular weight for $\text{C}_{288}\text{H}_{503}\text{N}_{82}\text{O}_{88}\text{S}_4$ having an average isotope composition is 6649.9. The ligated 4-helix TASP 3 was stable for days at ambient temperatures in pH 5.0 10mM NH_4OAc , and was indefinitely stable at 4°C at pH 6.0. Circular dichroism spectroscopy was used to determine the secondary structure of the ligated TASP molecule 3 in water. The molecule was highly helical (Figure 4). Control studies of peptide 1 under identical conditions showed no helical content whatever. These conformational properties were similar to those observed for the closely related 4-helix TASP prepared by conventional means (supra). Ionspray MS under native conditions¹⁷ showed that the 4-helix TASP occurred as a monomeric species, e.g., M. Baca et al.

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(*J. Am. Chem. Soc.*, 1992, vol. 114, pages 3992-3993).

The overwhelming feature of this synthetic approach is its simplicity. The ligation occurred rapidly in aqueous solution and essentially no other reaction products were detected. The product was readily purified to give exceptionally homogeneous material with a mass consistent with the proposed covalent structure. The observed helical secondary structure was consistent with the formation of the target 4-helix TASP molecule 3.

The major advantages of the chemoselective ligation approach include the elimination of microheterogeneity in the final product and the generality of the approach. Peptides simultaneously built up on the template by stepwise solid-phase synthesis yield very heterogeneous crude products. Mutter and co-workers have demonstrated the use of stringent chromatographic techniques to increase the purity of the final product (*supra*), but these protocols have not been applied to the larger and more hydrophobic ion channel assemblies prepared by Montal and co-workers (*Proc. Natl Acad. Sci. U.S.A.*, 1991, vol. 88, pages 6418-6422). Segment condensation of protected peptide fragments has been used to decrease heterogeneity but problems with solubility lead to extremely slow ligation reactions resulting in low yields. Recent work by DeGrado and co-workers used unprotected peptide fragments, but is of limited applicability due to the incompatibility of the ligation reaction with all functional groups, especially the ϵ -amino group of lysine (*J. Am. Chem. Soc.*, 1992, vol. 114, pages 9656-9657).

In contrast to these approaches, the chemoselective ligation approach allows ready purification of the unprotected peptide components, which can be ligated at high concentration in a fast, clean reaction. The target compound is obtained directly in the final unprotected form and is readily

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purified. The method is of general applicability because the chemistry is compatible with all functional groups found in peptides and proteins (Science, 1992, vol. 256, pages 221-225). In previous work we have shown that purified unprotected peptides can be correctly ligated in solvents such as 6 M guanidine HCl or in organic/aqueous mixtures. This allows great flexibility in the selection of pro-helix sequences and of solvent conditions to maintain the necessary solubility for rapid reaction.

Materials and Methods:

Analytical and semipreparative gradient HPLC was performed on a Rainin dual pump high pressure mixing system with 214 nm UV detection using Vydac C-18 analytical (5 micron, 0.46 x 15 cm) and semipreparative (10 m, 1.0 x 25 cm) columns. Analytical runs used a 0%-67% B gradient over 30 min at 1mL/min where buffer A is 0.1% TFA in H₂O and buffer B is 90% CH₃CN + 10% buffer A. Mass spectra were obtained using a Sciex API-III quadrupole ion-spray mass spectrometer. CD measurements were obtained using an Aviv 62 DS instrument. Peptide concentrations were determined by amino acid analysis after hydrolysis in 6 N HCl for 24 hours at 110°C.

Synthesis of pro-helix peptide 1. Except where noted, peptides were synthesized by manual stepwise solid phase methods according to published procedures, e.g., S. B. Kent (Ann Rev Biochem., 1988, vol. 57, pages 957-989) and M. Schnolzer et al. (Int. J. Peptide Protein Res., 1992, vol. 40, pages 180-193). Coupling yields were monitored by quantitative ninhydrin. The pro-helix was synthesized on a Gly thioester resin using standard N^{Boc} chemistry SPPS, e.g., J. Blake (Int. J. Peptide Protein Res., 1981, vol. 17, pages 273-274) and D. Yamashiro (J. Int. J. Peptide Protein Res., 1988, vol. 31, page 322). The peptide was deprotected and simultaneously cleaved from the resin

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by treatment with HF plus 2% anisole for 1 hour at 0°C. The crude peptide was taken up in neat TFA, diluted with ddH₂O to 0.5% TFA and lyophilized to remove residual anisole. The pro-helix was purified by semipreparative reversed phase HPLC (0%-67% buffer B over 60 min at 3 mL/min) and characterized by ionspray mass spectrometry, i.e., the observed molecular weight was 1372.2 ± 0.4 Daltons while the calculated molecular weight is 1371.8 daltons (monoisotopic) or 1372.6 daltons (average isotope composition).

Synthesis of template peptide 2. The template peptide was synthesized using a combination of N^tBoc-chemistry SPPS and N^tFmoc lysine side chain protection on a Gly-OCH₂-Pam-resin (Fig 1B). To minimize the possibility of premature Fmoc removal, a separate brief neutralization with 5% diisopropylethylamine/DMF was used, rather than *in situ* neutralization in the coupling step, e.g., M. Schnolzer et al. (*Int. J. Peptide Protein Res.*, 1992, vol. 40, pages 180-193). Following nine synthetic cycles, the Fmoc protecting groups on the lysine side chains were removed by two 5 minute treatments with 50% piperidine/DMF. The free ϵ -amino groups were bromoacetylated using bromoacetic acid/DIC coupling, e.g., R. A. Robey et al. (*Anal. Biochem.*, 1989, vol. 177, pages 373-377). The peptide was deprotected and cleaved by HF plus 10% *p*-cresol over 1h at 0°C, using standard protocols, e.g., M. Schnolzer et al. (*Int. J. Peptide Protein Res.*, 1992, vol. 40, pages 180-193). The template was then purified to homogeneity by semipreparative reversed phase HPLC (25%-41% buffer B over 30 minutes at 3mL/minute) and characterized by ionspray mass spectrometry, i.e., the observed molecular weight was 1482.7 ± 0.4 Daltons while the calculated molecular weight is 1478.3 daltons (monoisotopic) or 1483.0 daltons (average isotope composition).

Synthesis of 4-helix TASP 3. Ligation was

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performed by combining 0.50 mg of the (BrAc)₄ template (Formula weight 1484 Daltons, 3.36×10^{-7} mole, 1.12 mM), and 2.75 mg pro-helix-COSH (Formula weight 1372 Daltons, 2.0×10^{-6} mole, 6.68 mM) in 300 μ L of 10mM NH₄OAc aqueous buffer pH 5.0 at 23°C. Reaction was monitored by analytical reverse phase HPLC (4 μ L aliquots). Peaks were collected based on UV absorbance and examined by ionspray MS, e.g., M. Schnolzer (*Anal. Biochem.*, 1992, vol. 204, pages 335-343). After 6.5 hours at 23°C, the reaction mixture was stored at 4°C. Product (170 μ L of reaction mixture) was purified by reversed phase HPLC (38%-54% buffer B over 30 min at 3mL/minute) and lyophilized giving 0.26 mg of pure product, theoretical yield: 1.27mg, 20.5%. The mass was determined by ionspray mass spectrometry, i.e., the observed molecular weight was 6647.1 ± 2.8 Daltons while the calculated molecular weight is 6645.6 daltons (monoisotopic) or 6649.9 daltons (average isotope composition).

Stability. Stability was monitored by analytical reversed phase HPLC and mass spectrometry of collected peaks. 1 mM 4-helix TASP from the ligation reaction was stored at 23°C for several days without degradation. 5 mM 4-helix TASP stored in 100 mM Phosphate buffer pH 6.0 showed no decomposition after 7 days at 4°C.

Circular Dichroism. Both the pro-helix (7.5 μ M) and the 4-helix TASP (1.78 μ M) were dissolved in doubly distilled H₂O. Measurements were taken in a 2mL cuvette with a path length of 1cm at 20.0°C, scanning from 260nm to 190nm every 0.50 nm.

Conclusion

These results indicate the potential of the chemoselective ligation approach as a general route to the preparation of TASP-like macromolecules. Combinations of existing chemical tactics provide great versatility for the selective introduction of reactive

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moiety s into unprotected peptide building blocks which
can be used in the design and synthesis of a variety of
TASP-related compounds. In particular, the thioester
nucleophilic ligation chemistry described here can be
5 combined with other ligation chemistries originally
developed for rejoining fragments of proteins to
generate a great diversity of nonlinear covalent
molecular topologies, e.g., K. Rose et al.
(*Bioconjugate Chem.*, 1991, vol. 2, pages 154-159) and
10 H. Gaertner et al. (*Bioconjugate Chem.*, 1992, vol. 3,
pages 262-268). In conjunction with modern analytical
protein chemistry the chemoselective synthetic approach
is a powerful adjunct to the design and study of
conformations and activities of protein-related
15 macromolecules.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(ii) TITLE OF INVENTION: TEMPLATE ASSEMBLED SYNTHETIC PROTEIN

(iii) NUMBER OF SEQUENCES: 2

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
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- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(v) CURRENT APPLICATION DATE:

- (A) APPLICATION NUMBER: PCT/US/
- (B) FILING DATE: 11-AUG-1994

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/105,369
- (B) FILING DATE: 11-AUG-1993

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Thiolester-bond
- (B) LOCATION: 14
- (D) OTHER INFORMATION: /label= COS
/note= "COS indicates a thioester group on the
C-terminal amino acid."

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Asp Ala Ala Thr Ala Leu Ala Asn Ala Leu Lys Lys Leu Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 1

(D) OTHER INFORMATION: /label= Ac

/note= ""K(Ac) represents a lysine amino acid
residue having an lysine side chain with an
acetylated amino group.""

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 8

(D) OTHER INFORMATION: /label= Ac

/note= ""K(Ac) represents a lysine amino acid
residue having an lysine side chain with an
acetylated amino group.""

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Lys Lys Lys Pro Gly Lys Glu Lys Gly
1 5

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What is claimed is:

1. A template assembled synthetic protein (TASP) having a dendritic linkage unit with a structure $\psi(\text{CO-S-CH}_2\text{-CO-NH})$.

2. A template assembled synthetic protein (TASP) as described in claim 1 further comprising:

four dendritic linkage units having the structure $\psi(\text{CO-S-CH}_2\text{-CO-NH})$,

four branch peptides, each of said branch peptides having a sequence $^+\text{NH}_3\text{-D-A-A-T-A-L-A-N-A-L-K-K-L-G-COS-}$, and

a template peptide having a sequence $^+\text{NH}_3\text{-K(Ac-)-K(^+\text{NH}_3)\text{-K(Ac-)-P-G-K(Ac-)-E(COO^-)\text{-K(Ac-)-G-COO}^-}$,

said four linkage units coupling said branch peptides to the four K(Ac-) residues of said template peptide.

3. An improved template assembled synthetic protein (TASP) having a branch peptide with a C-terminal end and a template peptide including an amino acid residue with a template side chain bearing an amino group, wherein the improvement comprises:

a linkage unit having the structure $\psi(\text{CO-S-CH}_2\text{-CO-NH})$ coupling the C-terminal end of said branch peptide to said template peptide via the amino group of the template side chain as follows:

branch peptide- $\psi(\text{CO-S-CH}_2\text{-CO-NH})$ -template side chain

template peptide,

whereby the branch peptide serves as a branch upon the template peptide to form a template assembled synthetic protein (TASP).

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4. An improved template assembled synthetic protein (TASP) as described in claim 3 wherein:

the template side chain of said template peptide is a lysine side chain corresponding to a lysine amino acid residue.

5. An improved template assembled synthetic protein (TASP) as described in claim 3 wherein:

said branch peptide is a pro-helical peptide which, upon incorporation into the template assembled synthetic protein (TASP) and exposure to helix promoting conditions, is capable of assuming a helical configuration.

6. An improved template assembled synthetic protein (TASP) as described in claim 3 wherein the branch peptide includes a first branch peptide and a second branch peptide, each with a C-terminal end, and the template peptide includes a first amino acid residue with a first template side chain bearing an amino group and a second amino acid residue with a second template side chain bearing an amino group, wherein the improvement further comprises:

said linkage unit including a first linkage unit and a second linkage unit, each linkage unit having the structure $\psi(\text{CO-S-CH}_2\text{-CO-NH})$, the first linkage unit serving to couple the C-terminal end of said first branch peptide to said template peptide via the first template side chain and the second linkage unit serving to couple the C-terminal end of said second branch peptide to said template peptide via the second template side chain,

whereby the first and second branch peptides serve as first and second branches upon the template peptide to form a template assembled synthetic protein (TASP) having two branches.

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7. An improved template assembled synthetic protein (TASP) as described in claim 6 wherein:

5 both said first and second branch peptides are pro-helical peptides which, upon incorporation into the template assembled synthetic protein (TASP) and exposure to helix promoting conditions, are capable of assuming helical configurations.

10 8. A process for preparing a template assembled synthetic protein (TASP) comprising the following steps:

Step A: providing a template peptide including an amino acid residue having a template side chain bearing
15 an amino group bonded to a haloacetyl functionality;

Step B: providing one or more branch peptides, each of said branch peptides including a C-terminal end bearing an "COSH moiety; and then

20 Step C: combining the template peptide from said Step A with one or more of the branch peptides of said Step B under nucleophilic reaction conditions for promoting a substitution reaction between the "COSH moiety of the branch peptides and the haloacetyl functionality of the template molecule for
25 chemoselectively ligating the branch peptides to the template peptide and forming the template assembled synthetic protein (TASP).

30 9. A process for preparing a template assembled synthetic protein (TASP) as described in claim 8 wherein:

in said Step A, the haloacetyl functionality is a bromoacetyl functionality.

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10. A process for preparing a template assembled synthetic protein (TASP) as described in claim 9 wherein:

5 in said Step A, the template side chain bearing the amino group bonded to the haloacetyl functionality is a lysine side chain corresponding to a lysine amino acid residue.

10 11. A process for preparing a template assembled synthetic protein (TASP) as described in claim 8 wherein:

15 in said Step C, the C-terminal end of the branch peptide being ligated to the amino acid residue of the template peptide by means of a linkage unit having the structure $\psi(\text{CO-S-CH}_2\text{-CO-NH})$ to form the template assembled synthetic protein (TASP).

20 12. A process for preparing a template assembled synthetic protein (TASP) as described in claim 8 wherein:

25 in said Step B, the branch peptides are pro-helical peptides which, upon incorporation into the template assembled synthetic protein (TASP) and exposure to helix promoting conditions, are capable of assuming a helical configuration; and then, after or concurrent with Step C,

30 Step D: exposing the formed template assembled synthetic protein (TASP) of said Step C to helix promoting conditions for promoting the formation of helices by the branch peptides.

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FIG. 1A

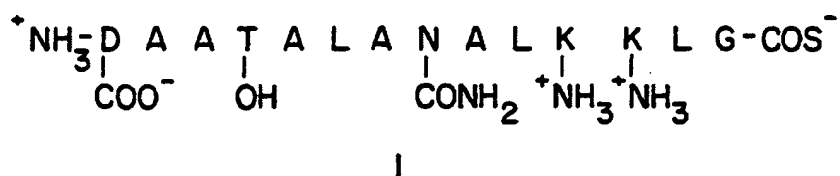
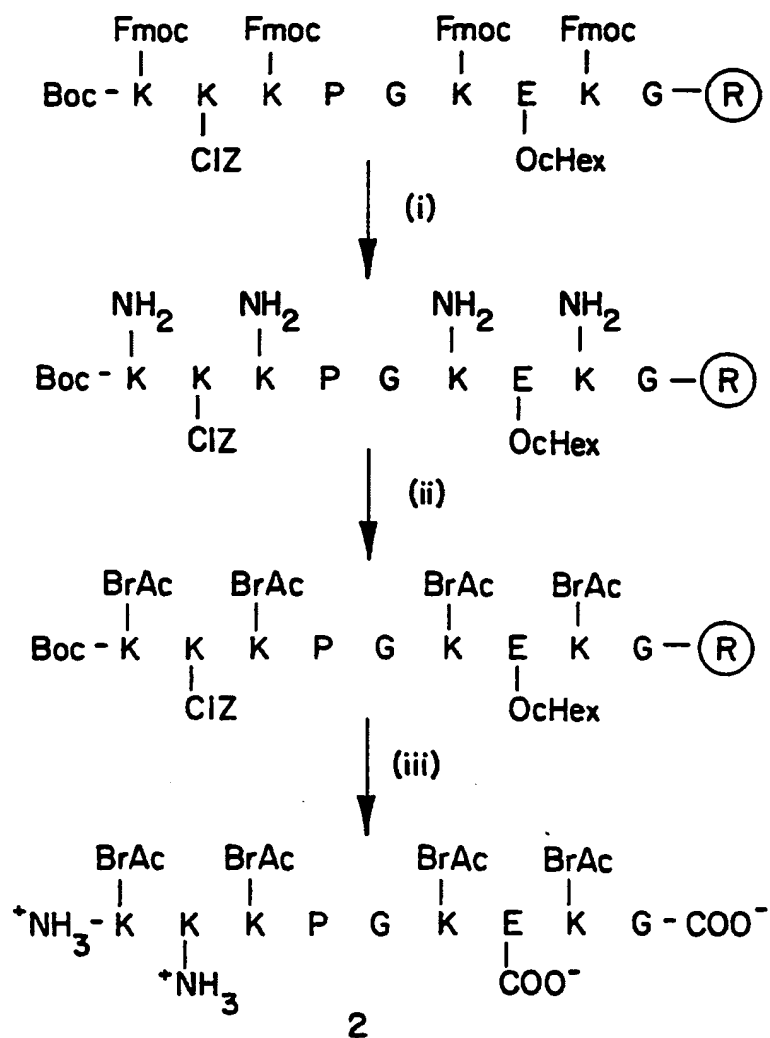


FIG. 1B



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FIG. 2A

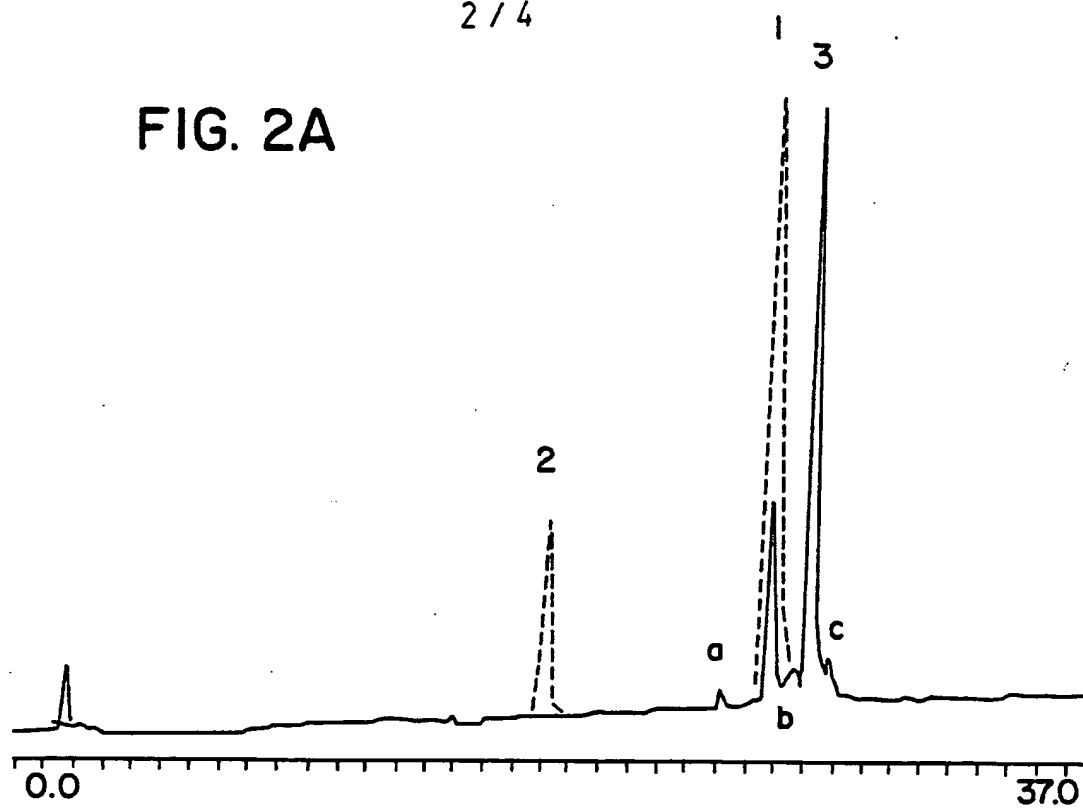
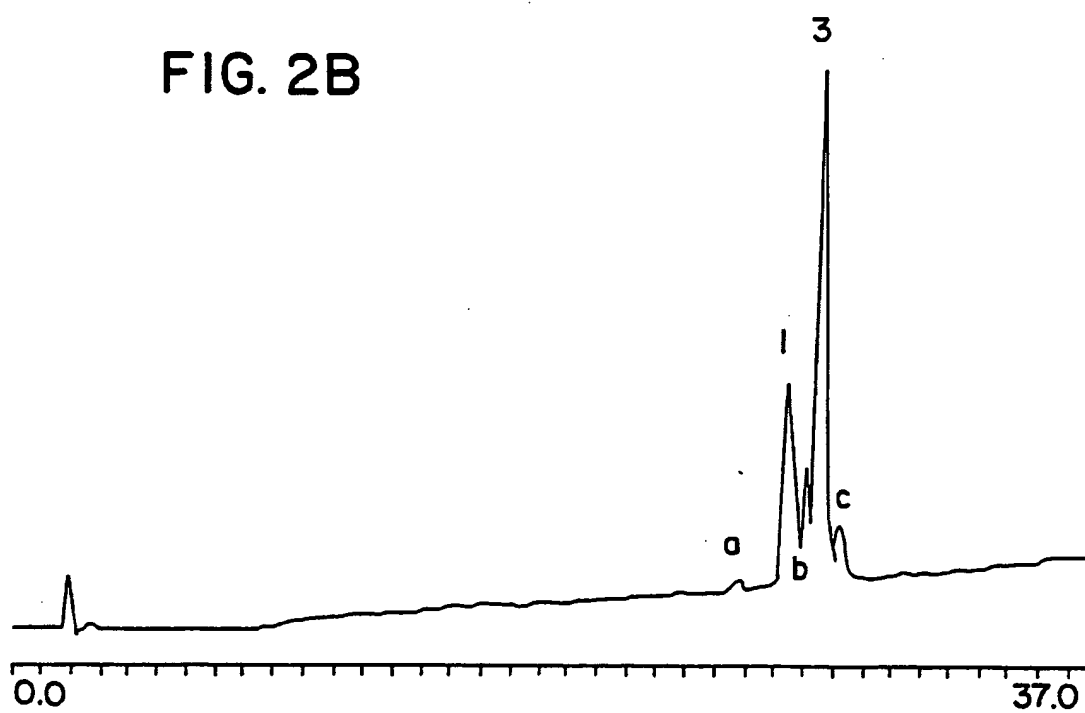
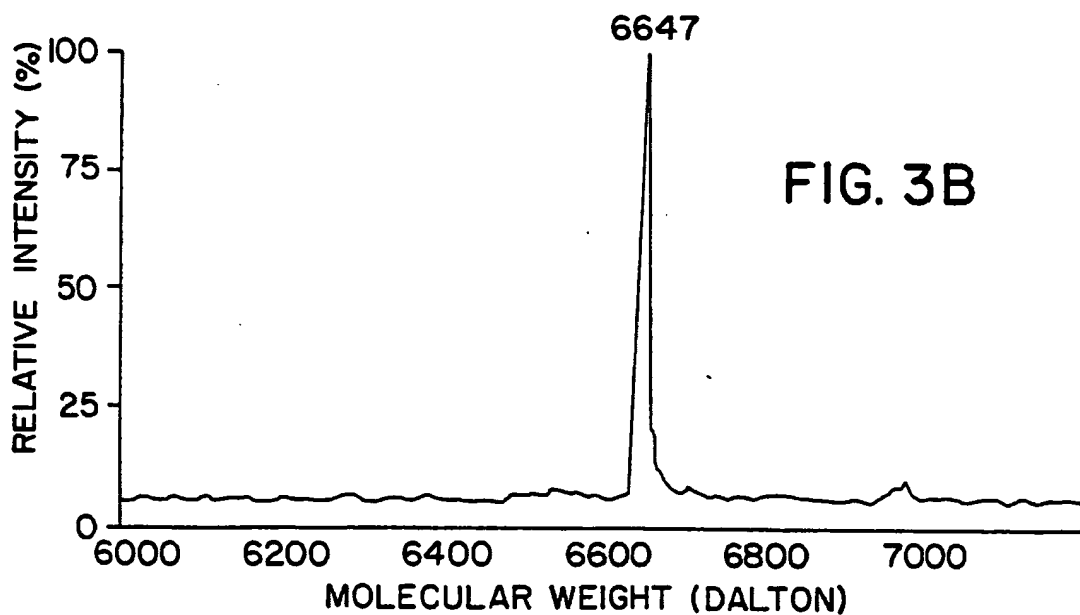
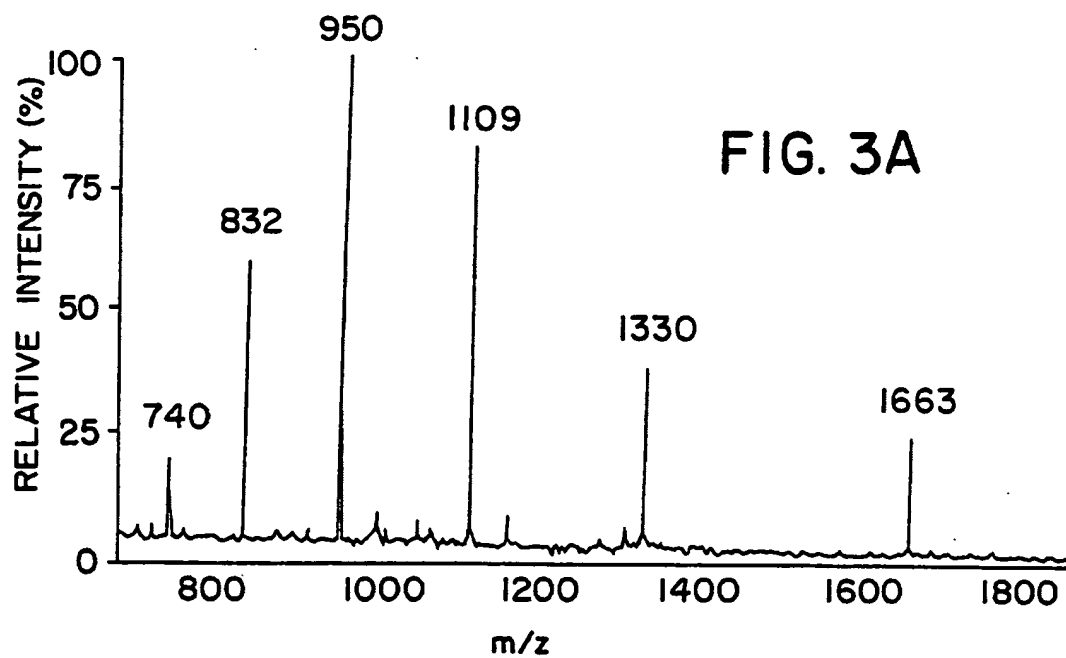


FIG. 2B



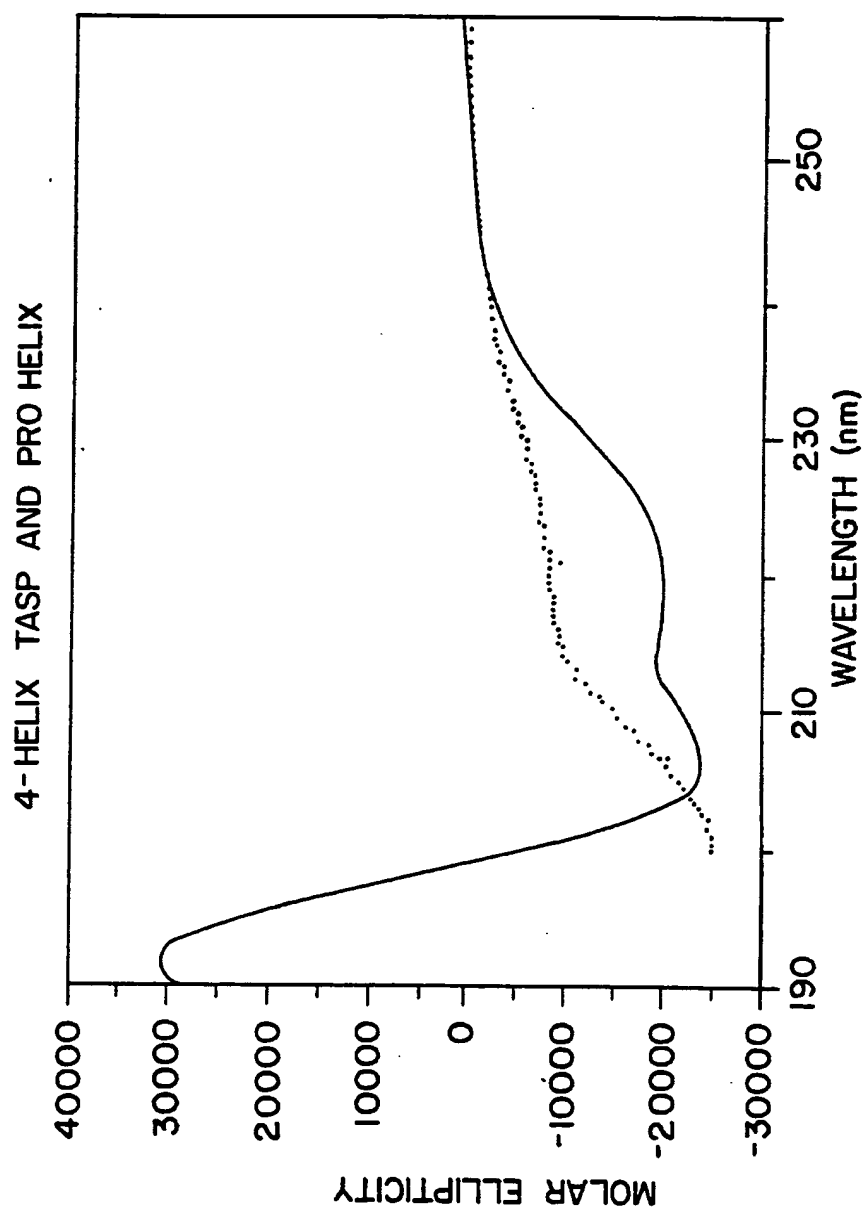
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FIG. 4



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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US94/09165

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :A61K 38/00

US CL :530/345

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 530/345, 333, 336, 324, 325

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

CAS Online

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	Angewante Chemie International Edition in English, Vol 28, No. 5, issued May 1989, M. Mutter et al., "A Chemical Approach to Protein Design- Template-Assembled Synthetic Proteins (TASP)", pages 535-554, see entire document.	1-12
A	US, A, 5,066,716 (ROBEY ET AL.) 19 November 1991, see entire document.	8-12

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

Special categories of cited documents:	
A document defining the general state of the art which is not considered to be of particular relevance	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
E earlier document published on or after the international filing date	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
O document referring to an oral disclosure, use, exhibition or other means	
P document published prior to the international filing date but later than the priority date claimed	*A* document member of the same patent family

Date of the actual completion of the international search

05 OCTOBER 1994

Date of mailing of the international search report

25 NOV 1994

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